



1653

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/455,978

Source: OIPF

Date Processed by STIC: 7/7/2001

RECEIVED

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/455,978

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

3 <110> APPLICANT: Alam, Maqsudul
 4 Larsen, Randy
 6 <120> TITLE OF INVENTION: HEME PROTEINS HEMAT-HS AND HEMAT-BS AND THEIR USE IN
 7 MEDICINE AND MICROSENSORS
 9 <130> FILE REFERENCE: 201040/1020
 11 <140> CURRENT APPLICATION NUMBER: 09/455,978
 12 <141> CURRENT FILING DATE: 1999-12-06
 14 <160> NUMBER OF SEQ ID NOS: 86
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1470
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Halobacterium salinarum
 23 <400> SEQUENCE: 1
 24 atgagcaacg ataatgacac tctcgtgacc gccgacgttc ggaacgggat cgacggggcac 60
 25 gcactcgcgg accggatcgg cctcgacgag gccgagatcg cgtggcggct gtcgttcacc 120
 26 gggatcgacg acgacacgat ggccgcgctc gccgccgaac agccgctgtt cgaagccacc 180
 27 gcggacgcgc tggtagccga cttctacgac cacttgaggt cctacgagcg cacacaggac 240
 28 ctcttcgcga actccacgaa gaccgtcgag caactcaaag agacgcaggc cgagtacttg 300
 29 ctgggcctcg ggccgcggcg gtacgacacc gactacgccg cccagcgcgc ccgtatcggg 360
 30 aagatacacg acgtgctcgg gctcggaccg gacgtctatc tgggcgcgta cacgcgatac 420
 31 tacacggggc tgttgacgc gcttgccgac gacgtggctc ccgaccgcgg cgaggaggcg 480
 32 gccgcgcggc tcgacgaact cgtggcccgg ttcttgccga tgttgaagct gttgaccttc 540
 33 gatcagcaga tcgcaatgga cacctacatc gactcgtacg cccagcgcct ccacgacgag 600
 34 atcgacagcc gccaggagtt ggcgacgcg gtcgccacgc acgtggaagc accgctgtcc 660
 35 tcgctggagg cgacctcgca ggacgtcgcc gagcgacgg acacgatgog ggcccgcacc 720
 36 gacgaccagg tcgaccgcat ggctgacgtc agccgtgaga tatccagcgt gtccgcgagc 780
 37 gtcgaggagg tcgcctcgac ggccgacgac gtccgcggga ccagcgagga cgccgaggcg 840
 38 ctggcccagc agggcgaggc ggccgcgcgac gacgcgctcg ccacgatgac cgacatcgac 900
 39 gaggcgaccg acggcgctcac cgcgggcgctc gaacagctcg gcgagcgcgc cgccgacgtc 960
 40 gaatcagtga ccggcgatgac cgacgacatc gccgagcaga cgaacatgct ggcgctgaac 1020
 41 gcgtccatcg agggcgcccg cgcgggggag gccggcgagg ggtttgcggt cgtcgccgac 1080
 42 gaggtcaagg ccctcgccga ggagtcccg gagcagtgca cgcgcgtcga ggagctcgtc 1140
 43 gagcagatgc aggcggagac cgaggagacg gtcgaccagt tggacgaggt caaccagcgc 1200
 44 atcggcgagg gcgtcgagcg cgtcgaggag gcgatggaga ccctccagga gatcaccgac 1260
 45 gccgtcgagg acgcccgaag cgggatgcag gaggtgtcga cggcgaccga cgaacaggcg 1320
 46 gtgagcaccg aggaggtcgc cgagatggtc gacggtgtcg acgaccgcgc gggcgagatc 1380
 47 gcggccgccc tcgatgacat cgccgacgcg accgatcagc aggtccggac cgtcgaggag 1440
 48 gtccgcgaga cggtcggcaa gctcagctag 1470
 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 489
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Halobacterium salinarum
 56 <400> SEQUENCE: 2
 57 Met Ser Asn Asp Asn Asp Thr Leu Val Thr Ala Asp Val Arg Asn Gly
 58 1 5 10 15
 60 Ile Asp Gly His Ala Leu Ala Asp Arg Ile Gly Leu Asp Glu Ala Glu

Does Not Comply
 Corrected Diskette Needed

see page 5

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DATE: 07/07/2001

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Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

```

61      20      25      30
63 Ile Ala Trp Arg Leu Ser Phe Thr Gly Ile Asp Asp Asp Thr Met Ala
64      35      40      45
66 Ala Leu Ala Ala Glu Gln Pro Leu Phe Glu Ala Thr Ala Asp Ala Leu
67      50      55      60
69 Val Thr Asp Phe Tyr Asp His Leu Glu Ser Tyr Glu Arg Thr Gln Asp
70      65      70      75      80
72 Leu Phe Ala Asn Ser Thr Lys Thr Val Glu Gln Leu Lys Glu Thr Gln
73      85      90      95
75 Ala Glu Tyr Leu Leu Gly Leu Gly Arg Gly Glu Tyr Asp Thr Glu Tyr
76      100      105      110
78 Ala Ala Gln Arg Ala Arg Ile Gly Lys Ile His Asp Val Leu Gly Leu
79      115      120      125
81 Gly Pro Asp Val Tyr Leu Gly Ala Tyr Thr Arg Tyr Tyr Thr Gly Leu
82      130      135      140
84 Leu Asp Ala Leu Ala Asp Asp Val Val Ala Asp Arg Gly Glu Glu Ala
85      145      150      155      160
87 Ala Ala Ala Val Asp Glu Leu Val Ala Arg Phe Leu Pro Met Leu Lys
88      165      170      175
90 Leu Leu Thr Phe Asp Gln Gln Ile Ala Met Asp Thr Tyr Ile Asp Ser
91      180      185      190
93 Tyr Ala Gln Arg Leu His Asp Glu Ile Asp Ser Arg Gln Glu Leu Ala
94      195      200      205
96 Asn Ala Val Ala Thr His Val Glu Ala Pro Leu Ser Ser Leu Glu Ala
97      210      215      220
99 Thr Ser Gln Asp Val Ala Glu Arg Thr Asp Thr Met Arg Ala Arg Thr
100      225      230      235      240
102 Asp Asp Gln Val Asp Arg Met Ala Asp Val Ser Arg Glu Ile Ser Ser
103      245      250      255
105 Val Ser Ala Ser Val Glu Glu Val Ala Ser Thr Ala Asp Asp Val Arg
106      260      265      270
108 Arg Thr Ser Glu Asp Ala Glu Ala Leu Ala Gln Gln Gly Glu Ala Ala
109      275      280      285
111 Ala Asp Asp Ala Leu Ala Thr Met Thr Asp Ile Asp Glu Ala Thr Asp
112      290      295      300
114 Gly Val Thr Ala Gly Val Glu Gln Leu Gly Glu Arg Ala Ala Asp Val
115      305      310      315      320
117 Glu Ser Val Thr Gly Val Ile Asp Asp Ile Ala Glu Gln Thr Asn Met
118      325      330      335
120 Leu Ala Leu Asn Ala Ser Ile Glu Ala Ala Arg Ala Gly Glu Ala Gly
121      340      345      350
123 Glu Gly Phe Ala Val Val Ala Asp Glu Val Lys Ala Leu Ala Glu Glu
124      355      360      365
126 Ser Arg Glu Gln Ser Thr Arg Val Glu Glu Leu Val Glu Gln Met Gln
127      370      375      380
129 Ala Glu Thr Glu Glu Thr Val Asp Gln Leu Asp Glu Val Asn Gln Arg
130      385      390      395      400
132 Ile Gly Glu Gly Val Glu Arg Val Glu Glu Ala Met Glu Thr Leu Gln
133      405      410      415

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Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

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135 Glu Ile Thr Asp Ala Val Glu Asp Ala Ala Ser Gly Met Gln Glu Val
136           420           425           430
138 Ser Thr Ala Thr Asp Glu Gln Ala Val Ser Thr Glu Glu Val Ala Glu
139           435           440           445
141 Met Val Asp Gly Val Asp Asp Arg Ala Gly Glu Ile Ala Ala Ala Leu
142           450           455           460
144 Asp Asp Ile Ala Asp Ala Thr Asp Gln Gln Val Arg Thr Val Glu Glu
145 465           470           475           480
147 Val Arg Glu Thr Val Gly Lys Leu Ser
148           485
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 1390
153 <212> TYPE: DNA
154 <213> ORGANISM: Bacillus subtilis
156 <400> SEQUENCE: 3
157 atgttatttta aaaaagacag aaaacaagaa acagcttact tttcagattc aaacggacaa 60
158 caaaaaaacc gcattcagct cacaacaaca catgcagatg tcaaaaaaca gctcaaaatg 120
159 gtcagggttg gagatgctga gctttatgtg ttagagcagc ttcagccact cattcaagaa 180
160 aatatcgtaa atatcgtcga tgcgttttat aaaaaccttg accatgaaag ctcatgatg 240
161 gatatcatta atgatcacag ctcatgtgac cgcttaaaac aaacgttaaa acggcatatt 300
162 caggaaatgt ttgcaggcgt tatcgatgat gaatttattg aaaagcgtaa ccgaatcgcc 360
163 tccatccatt taagaatcgg ccttttgcca aaatggtata tgggtgcgtt tcaagagctc 420
164 cttttgtcaa tgattgacat ttatgaagcg tccattacaa atcagcaaga actgctaaaa 480
165 gccattaaag caacaacaaa aatcttgaac ttagaacagc agcttgtcct tgaagcgttt 540
166 caaagcgagt acaaccagac ccgtgatgaa caagaagaaa agaaaaacct tcttcatcag 600
167 aaaattcaag aaacctctgg atcgattgcc attctgtttt cagaaacaag cagatcagtt 660
168 caagagcttg tggacaaatc tgaaggcatt tctcaagcat ccaaagccgg cactgtaaca 720
169 tccagcactg ttgaagaaaa gtcgatcggc ggaaaaaaag agctagaagt ccagcaaaaa 780
170 cagatgaaca aaattgacac aagccttgtc caaatcgaaa aagaaatggt caagctggat 840
171 gaaatcgcgc agcaaattga aaaaatcttc ggcacgtcga caggcatagc tgaacaaaca 900
172 aaccttctct cgtcfaatgc atctattgaa tccgcccgcg ccggagaaca cggcaaaggc 960
173 tttgctgtcg tggcaaatga agtgcggaag ctttctgagg atacgaaaaa aaccgtctct 1020
174 actgtttctg agcttgtgaa caatacgaat acacaaatca acattgtatc caagcatatc 1080
175 aaagacgtga atgagctagt cagcgaaagt aaagaaaaaa tgacgcaaat taaccgctta 1140
176 ttcgatgaaa tcgtccacag catgaaaatc agcaaagagc aatcaggcaa aatcgacgtc 1200
177 gatctgcaag ctttcttgagg agggcttcag gaagtcagcc gcgccgtttc ccatgtggcc 1260
178 gcttccggtt attcgcttgt catcctgaca gaagaataac catcaaaaac cggcttgcca 1320
179 tacggccggt ttttttgcgt tcattatgta aacttaaatt aaaaatcagt tgacataata 1380
180 attacctgca
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 432
185 <212> TYPE: PRT
186 <213> ORGANISM: Bacillus subtilis
188 <400> SEQUENCE: 4
189 Met Leu Phe Lys Lys Asp Arg Lys Gln Glu Thr Ala Tyr Phe Ser Asp
190 1 5 10 15
192 Ser Asn Gly Gln Gln Lys Asn Arg Ile Gln Leu Thr Asn Lys His Ala
193 20 25 30
195 Asp Val Lys Lys Gln Leu Lys Met Val Arg Leu Gly Asp Ala Glu Leu

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Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

```

196          35          40          45
198 Tyr Val Leu Glu Gln Leu Gln Pro Leu Ile Gln Glu Asn Ile Val Asn
199          50          55          60
201 Ile Val Asp Ala Phe Tyr Lys Asn Leu Asp His Glu Ser Ser Leu Met
202 65          70          75          80
204 Asp Ile Ile Asn Asp His Ser Ser Val Asp Arg Leu Lys Gln Thr Leu
205          85          90          95
207 Lys Arg His Ile Gln Glu Met Phe Ala Gly Val Ile Asp Asp Glu Phe
208          100          105          110
210 Ile Glu Lys Arg Asn Arg Ile Ala Ser Ile His Leu Arg Ile Gly Leu
211          115          120          125
213 Leu Pro Lys Trp Tyr Met Gly Ala Phe Gln Glu Leu Leu Leu Ser Met
214          130          135          140
216 Ile Asp Ile Tyr Glu Ala Ser Ile Thr Asn Gln Glu Leu Leu Lys
217 145          150          155          160
219 Ala Ile Lys Ala Thr Lys Ile Leu Asn Leu Glu Gln Gln Leu Val
220          165          170          175
222 Leu Glu Ala Phe Gln Ser Glu Tyr Asn Gln Thr Arg Asp Glu Gln Glu
223          180          185          190
225 Glu Lys Lys Asn Leu Leu His Gln Lys Ile Gln Glu Thr Ser Gly Ser
226          195          200          205
228 Ile Ala Asn Leu Phe Ser Glu Thr Ser Arg Ser Val Gln Glu Leu Val
229          210          215          220
231 Asp Lys Ser Glu Gly Ile Ser Gln Ala Ser Lys Ala Gly Thr Val Thr
232 225          230          235          240
234 Ser Ser Thr Val Glu Glu Lys Ser Ile Gly Gly Lys Lys Glu Leu Glu
235          245          250          255
237 Val Gln Gln Lys Gln Met Asn Lys Ile Asp Thr Ser Leu Val Gln Ile
238          260          265          270
240 Glu Lys Glu Met Val Lys Leu Asp Glu Ile Ala Gln Gln Ile Glu Lys
241          275          280          285
243 Ile Phe Gly Ile Val Thr Gly Ile Ala Glu Gln Thr Asn Leu Leu Ser
244          290          295          300
246 Leu Asn Ala Ser Ile Glu Ser Ala Arg Ala Gly Glu His Gly Lys Gly
247 305          310          315          320
249 Phe Ala Val Val Ala Asn Glu Val Arg Lys Leu Ser Glu Asp Thr Lys
250          325          330          335
252 Lys Thr Val Ser Thr Val Ser Glu Leu Val Asn Asn Thr Asn Thr Gln
253          340          345          350
255 Ile Asn Ile Val Ser Lys His Ile Lys Asp Val Asn Glu Leu Val Ser
256          355          360          365
258 Glu Ser Lys Glu Lys Met Thr Gln Ile Asn Arg Leu Phe Asp Glu Ile
259          370          375          380
261 Val His Ser Met Lys Ile Ser Lys Glu Gln Ser Gly Lys Ile Asp Val
262 385          390          395          400
264 Asp Leu Gln Ala Phe Leu Gly Gly Leu Gln Glu Val Ser Arg Ala Val
265          405          410          415
267 Ser His Val Ala Ala Ser Val Asp Ser Leu Val Ile Leu Thr Glu Glu
268          420          425          430

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TIME: 13:15:00

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

```

274 <210> SEQ ID NO: 5
275 <211> LENGTH: 57
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Template
281     sequence
283 <220> FEATURE:
284 <221> NAME/KEY: UNSURE
285 <222> LOCATION: (4)
286 <223> OTHER INFORMATION: X at any position in this sequence is unknown.
288 <400> SEQUENCE: 5
W--> 289 Ile Ile Lys Xaa Thr Val Pro Val Leu Xaa Glu His Gly Xaa Xaa Ile
      290   1       5           10           15
W--> 292 Gly Gln Asp Val Leu Val Val Leu Ile Lys Xaa Asn Pro Glu Ile Gln
      293       20           25           30
W--> 295 Glu Lys Phe Phe Phe Lys His Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      296       35           40           45
W--> 298 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      299       50           55
302 <210> SEQ ID NO: 6
303 <211> LENGTH: 55
304 <212> TYPE: PRT
305 <213> ORGANISM: Erwinia chrysanthemi
307 <400> SEQUENCE: 6
308 Ile Lys Ser Thr Ile Pro Leu Leu Ala Glu Thr Gly Pro Ala Leu Thr
309   1       5           10           15
311 Ala His Phe Tyr Gln Arg Met Phe His His Asn Pro Glu Leu Lys Asp
312       20           25           30
314 Ile Phe Asn Met Ser Asn Gln Arg Asn Gly Asp Gln Arg Glu Ala Leu
315       35           40           45
317 Phe Asn Ala Ile Cys Ala Tyr
318       50           55
321 <210> SEQ ID NO: 7
322 <211> LENGTH: 56
323 <212> TYPE: PRT
324 <213> ORGANISM: Vitreoscilla stercoraria
326 <400> SEQUENCE: 7
327 Ile Ile Lys Ala Thr Val Pro Val Leu Lys Glu His Gly Val Thr Ile
328   1       5           10           15
330 Thr Thr Thr Phe Tyr Lys Asn Leu Phe Ala Lys His Pro Glu Val Arg
331       20           25           30
333 Pro Leu Phe Asp Met Gly Arg Gln Glu Ser Leu Glu Gln Pro Lys Ala
334       35           40           45
336 Leu Ala Met Thr Val Leu Ala Ala
337       50           55
340 <210> SEQ ID NO: 8
341 <211> LENGTH: 55
342 <212> TYPE: PRT

```

*<222> must contain location of all Xaa's.
If Xaa's are all the same use of a range
to describe the location is fine. See item #5
on Error
Summary
Sheet*

FYI:

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/455,978

DATE: 07/07/2001

TIME: 13:15:01

Input Set : A:\H1020011.app

Output Set: N:\CRF3\07062001\I455978.raw

L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:1703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
L:1744 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:1763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
L:1785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86